

OM protein - protein search, using sw model

Run on: September 28, 2001, 12:26:05 ; Search time 53.45 Seconds
(without alignments)
6,409 Million cell updates/sec

Title: US-09-551-645-1
Perfect score: 49
Sequence: 1 TFIGATATDT 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	1645	1	OMP.B_RICTY
2	48	98.0	1643	1	OMP.B_RICPR
3	39	79.6	1300	1	120K_RICRI
4	39	79.6	1654	1	OMP.B_RICRI
5	36	73.5	174	1	CHCB_BOOMO
6	35	71.4	1254	1	YNCA_CAEEL
7	35	71.4	1656	1	OMP.B_RICJA
8	33	67.3	106	1	YCDZ_SALTY
9	33	67.3	179	1	THM1_ARATH
10	33	67.3	179	1	YCDZ_ECOCI
11	33	67.3	292	1	DHBD_ASPNG
12	33	67.3	531	1	C7E1_SORBI
13	33	67.3	553	1	HIS5_EMENI
14	32	65.3	167	1	CHCC_ANTPO
15	32	65.3	317	1	MSHR_BOVIN
16	32	65.3	317	1	MSHR_CANFA
17	32	65.3	317	1	MSHR_CANFA
18	32	65.3	317	1	MSHR_CANFA
19	32	65.3	317	1	MSHR_CEREL
20	32	65.3	317	1	MSHR_DANDA
21	32	65.3	317	1	MSHR_HUMAN
22	32	65.3	317	1	MSHR_OVIMO
23	32	65.3	317	1	MSHR_RANTA
24	32	65.3	317	1	MSHR_SHEEP
25	32	65.3	317	1	MSHR_VILVU
26	32	65.3	355	1	CAPH_STAUV
27	32	65.3	540	1	P39857 STAPHYLOCO
28	31	63.3	317	1	MSHR_ECOCI
29	31	63.3	362	1	MSHR_ALCAA
30	31	63.3	392	1	YD33_MYCLE
31	31	63.3	392	1	CMR_SPRLI
32	31	63.3	427	1	Y686_CHLTR
33	31	63.3	716	1	V88_MTV
					RPR1_DHV11
					P27153 dhori virus

ALIGNMENTS

RESULT 1	OMP.B_RICTY	STANDARD	PRT: 1645 AA.
AC	P96989;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)		
DE	(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)		
DE	(CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)		
DE	(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).		
GN	SLP.		
OS	Rickettsia typhi.		
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;		
OC	Rickettsiaceae; Rickettsiae; Rickettsia.		
OX	NCBI_Taxid=785;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RE	STRAIN-WILMINGTON.		
RX	MEDLINE=94040787; PubMed=8224886;		
RA	Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;		
RT	*Cloning and sequence analysis of the gene encoding the crystalline		
RT	surface layer protein of Rickettsia typhi.*		
RL	Gene 133:129-133(1993)		
RM	[2]		
RP	PARTIAL SEQUENCE.		
RC	STRAIN-WILMINGTON.		
RX	MEDLINE=92114896; PubMed=1370573;		
RA	Ching W.M., Carl M., Dasch G.A.;		
RT	*Mapping of monoclonal antibody binding sites on CNR fragments of		
RT	the S-layer protein antigens of Rickettsia typhi and Rickettsia		
RT	proweazekii.*		
RL	Mol. Immunol. 29:95-105(1992).		
RN	[3]		
RP	IDENTIFICATION OF CLEAVAGE SITE.		
RX	MEDLINE=92104668; PubMed=1729180;		
RA	Hackstadt T., Messer R., Cleplak W., Peacock M.G.;		
RT	*Evidence for proteolytic cleavage of the 120-kilodalton outer		
RT	membrane protein of Rickettsiae: Identification of an avirulent		
RT	mutant deficient in processing.*		
RL	Infect. Immun. 60:159-165(1992).		
CC	- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR		
CC	STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL		
CC	VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.		
CC	- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.		
CC	SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A		
CC	S-LAYER WITH HEXAGONAL SYMMETRY.		
CC			
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Seq 10 NO.1

DR EMBL: L04661; AAB48987.1; -
 KW Antigen: S-layer; Transmembrane; Cell wall.
 FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
 FT TRANSMEM 1415 1645 32 KDA BETA PEPTIDE.
 FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
 FT CONFLICT 657 657 H -> N (IN REF. 2).
 FT CONFLICT 842 842 V -> I (IN REF. 2).
 FT CONFLICT 1071 1071 G -> A (IN REF. 2).
 FT CONFLICT 1306 1306 G -> S (IN REF. 2).
 SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7ED185EE CRC64;

Query Match 100.0%; Score 49; DB 1; Length 1645;
 Best Local Similarity 100.0%; Pred. No. 0.048;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TFGAIADT 10
 Db 1296 TFGAIADT 1305

RESULT 2

OMP_RICPR STANDARD; PRT: 1643 AA.
 AC 053020; Q9ZCM0;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
 DE (SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
 DE (CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
 DE (120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
 OS OMPB OR SPAP OR SPA OR RP704
 OC Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiense; Rickettsia.
 OC NCBI_TaxID=782;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-BREINL.
 RA MEDLINE-91045972; PubMed-2122457;
 RA Carl M., Dobson M.E., Ching W.M., Dasch G.A.;
 RT "Characterization of the gene encoding the protective paracrystalline-
 RT surface-layer protein of Rickettsia prowazekii: presence of a
 RT truncated identical homolog in Rickettsia typhi."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BREINL.
 RA Moron C.G., Yu X.J., Walker D.H.;
 RT "Sequence analysis of ompb of Rickettsia prowazekii."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RA MEDLINE-99039499; PubMed-9823893;
 RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
 RA Slicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria."
 RL Nature 396:133-140(1998).
 RN [4]
 RP PARTIAL SEQUENCE.
 RC STRAIN-BREINL.
 RA MEDLINE-92114896; PubMed-1370573;
 RA Ching W.M., Carl M., Dasch G.A.;
 RT "Mapping of monoclonal antibody binding sites on CNB: fragments of
 RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
 RT prowazekii."
 RL Mol. Immunol. 29:95-105(1992).
 RN [5]

RX MEDLINE-92104668; PubMed-1729180;
 RA Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
 RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
 RT membrane protein of rickettsiae: identification of an avirulent mutant
 RT deficient in processing."
 RL Infect. Immun. 60:159-165(1992).
 CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: M37647; AAA26390.1; ALT_INIT.
 DR EMBL: A161079; AAD42234.1; -
 DR EMBL: A1235273; CAAL5140.1; -
 KW Antigen: S-layer; Cell wall.
 FT CHAIN 1 1328 120 KDA SURFACE-EXPOSED PROTEIN.
 FT VARIANT 1329 1643 32 KDA BETA PEPTIDE.
 FT VARIANT 1329 1643 V -> A (IN STRAIN BREINL).
 FT VARIANT 1010 1010 Y -> D (IN STRAIN BREINL).
 FT VARIANT 1490 1450 A -> S (IN STRAIN BREINL).
 FT CONFLICT 178 179 AA -> VC (IN REF. 1).
 FT CONFLICT 191 201 T -> I (IN REF. 1).
 FT CONFLICT 212 212 T -> L (IN REF. 1).
 FT CONFLICT 313 313 D -> G (IN REF. 1).
 FT CONFLICT 1104 1104 T -> S (IN REF. 2).
 FT CONFLICT 1123 1123
 SQ SEQUENCE 1643 AA; 169854 MW; 735FDF392E6346CC CRC64;

Query Match 98.0%; Score 48; DB 1; Length 1643;
 Best Local Similarity 90.0%; Pred. No. 0.077;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TFGAIADT 10
 Db 1296 TFGAIADT 1305

RESULT 3
 ID 120K_RICRI STANDARD; PRT: 1300 AA.
 AC P14914;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE 120 KDA SURFACE-EXPOSED PROTEIN.
 GN P120.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiense; Rickettsia.
 OC NCBI_TaxID=783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R.
 RA MEDLINE-90136087; PubMed-2515418;
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
 RT "Cloning, expression and sequence analysis of the gene encoding the
 RT 120 kD surface-exposed protein of Rickettsia rickettsii."
 RL Mol. Microbiol. 3:1579-1586(1989).
 CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
 CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
 CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-